

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

101820,067
TEUB
1-31-05

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/820/007

ATTN: NEW RULES CASES: PLEASE DISREGARD ENCL[II]-ALPIIA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

1 **Wrapped Nucleic** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>..<223> section that some may be missing.

6 **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>..<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>..<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>..<223> sections for Artificial or Unknown sequences.

7 **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

8 **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>..<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence or scientific name (Genus/species). <220>..<223> section is required when <213> response is Unknown.

11 **Use of <220>** Sequence(s) _____ use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/820,067

DATE: 01/31/2005
TIME: 11:27:02

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

4 <110> APPLICANT: Fletchner, J.
5 Prince-Cohane, K.
6 Mehta, S.
7 Slusarewicz, P.
8 Andjelic, S.
9 Barber, B.
11 <120> TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
12 VACCINES AND IMMUNOTHERAPIES
15 <130> FILE REFERENCE: 8449-406-999
17 <140> CURRENT APPLICATION NUMBER: 10/820,067
18 <141> CURRENT FILING DATE: 2004-04-08
20 <150> PRIOR APPLICATION NUMBER: 60/462,469
21 <151> PRIOR FILING DATE: 2003-04-11
23 <150> PRIOR APPLICATION NUMBER: 60/463,746
24 <151> PRIOR FILING DATE: 2003-04-18
26 <150> PRIOR APPLICATION NUMBER: 60/503,417
27 <151> PRIOR FILING DATE: 2003-09-16
29 <160> NUMBER OF SEQ ID NOS: 926
31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 4
35 <212> TYPE: PRT
36 <213> ORGANISM: Malaria
38 <400> SEQUENCE: 1
39 Asn Ala Asn Pro
40 1
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 9
45 <212> TYPE: PRT
46 <213> ORGANISM: Unknown
48 <220> FEATURE:
49 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 51 <221> NAME/KEY: VARIANT
52 <222> LOCATION: 2
53 <223> OTHER INFORMATION: Xaa = Leu or Met
W--> 55 <221> VARIANT
56 <222> LOCATION: 6
57 <223> OTHER INFORMATION: Xaa = Val or Ile or Leu or Thr
W--> 59 <221> VARIANT
60 <222> LOCATION: 9
61 <223> OTHER INFORMATION: Xaa = Val or Leu
W--> 63 <221> VARIANT
64 <222> LOCATION: 1,3 , 4, 5, 7, 8

Does Not Comply
Corrected Diskette Needed

(pg. 23)

RAW SEQUENCE LISTING
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Input Set : D:\SEQLIST 8449-406 (as filed).TXT
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65 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 67 <400> 2
W--> 68 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
69 1 5
72 <210> SEQ ID NO: 3
73 <211> LENGTH: 9
74 <212> TYPE: PRT
75 <213> ORGANISM: Unknown
77 <220> FEATURE:
78 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 80 <221> NAME/KEY: VARIANT
81 <222> LOCATION: 2
82 <223> OTHER INFORMATION: Xaa = Leu or Met
W--> 84 <221> VARIANT
85 <222> LOCATION: 1, 3, 4, 5, 6, 7, 8
86 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 88 <400> 3
W--> 89 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
90 1 5
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 8
95 <212> TYPE: PRT
96 <213> ORGANISM: Unknown
98 <220> FEATURE:
99 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 101 <221> NAME/KEY: VARIANT
102 <222> LOCATION: 2
103 <223> OTHER INFORMATION: Xaa = Val or Gln
W--> 105 <221> VARIANT
106 <222> LOCATION: 1, 3, 4, 5, 6, 7, 8 *Leu is at this location*
107 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 109 <400> 4
W--> 110 Xaa Xaa Xaa Xaa Xaa Xaa Leu
111 1 5
114 <210> SEQ ID NO: 5
115 <211> LENGTH: 5
116 <212> TYPE: PRT
117 <213> ORGANISM: Unknown
119 <220> FEATURE:
120 <223> OTHER INFORMATION: HLA-DR peptide binding motif
122 <400> SEQUENCE: 5
123 Gln Lys Arg Ala Ala
124 1 5
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 5
129 <212> TYPE: PRT
130 <213> ORGANISM: Unknown
132 <220> FEATURE:
133 <223> OTHER INFORMATION: HLA-DR peptide binding motif

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/820,067

DATE: 01/31/2005
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Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

135 <400> SEQUENCE: 6
136 Arg Arg Arg Ala Ala
137 1 5
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 7
142 <212> TYPE: PRT
143 <213> ORGANISM: Unknown
145 <220> FEATURE:
146 <223> OTHER INFORMATION: motif in heptameric region recognized by heat
147 shock protein
W--> 149 <221> NAME/KEY: VARIANT
150 <222> LOCATION: 2
151 <223> OTHER INFORMATION: Xaa = Trp or any amino acid
W--> 153 <221> VARIANT
154 <222> LOCATION: 1, 3, 5, 7
155 <223> OTHER INFORMATION: Xaa = hydrophobic amino acid residues
W--> 157 <221> VARIANT
158 <222> LOCATION: 4, 6
159 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 161 <400> 7
W--> 162 Xaa Xaa Xaa Xaa Xaa Xaa
163 1 5
166 <210> SEQ ID NO: 8
167 <211> LENGTH: 7
168 <212> TYPE: PRT
169 <213> ORGANISM: Unknown
171 <220> FEATURE:
172 <223> OTHER INFORMATION: motif in heptameric region recognized by heat
173 shock protein
W--> 175 <221> NAME/KEY: VARIANT
176 <222> LOCATION: 2
177 <223> OTHER INFORMATION: Xaa = Trp or any amino acid
W--> 179 <221> VARIANT
180 <222> LOCATION: 1, 3, 5, 7,
181 <223> OTHER INFORMATION: Xaa = hydrophobic amino acid residue, particularly
182 tryptophan, leucine or phenylalanine
W--> 184 <221> VARIANT
185 <222> LOCATION: 4, 6
186 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 188 <400> 8
W--> 189 Xaa Xaa Xaa Xaa Xaa Xaa
190 1 5
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 4
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <221> NAME/KEY: VARIANT
200 <222> LOCATION: 1

See item # 11 on error
summary sheet

pls explain source
of genetic material.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING

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Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

201 <223> OTHER INFORMATION: Xaa = Ala/Ser/Val/Lys/Glu/Gly/Leu
203 <220> FEATURE:
204 <223> OTHER INFORMATION: In the order of preference, with Ala the most preferred
206 <220> FEATURE:
207 <221> NAME/KEY: VARIANT
208 <222> LOCATION: 2
209 <223> OTHER INFORMATION: Xaa = Lys/Val/Glu
211 <220> FEATURE:
212 <223> OTHER INFORMATION: In the order of preference, with Lys the most preferred
214 <220> FEATURE:
215 <221> NAME/KEY: VARIANT
216 <222> LOCATION: 3
217 <223> OTHER INFORMATION: Xaa = Val/Ser/Phe/Thr/Lys/Ala/Glu
219 <220> FEATURE:
220 <223> OTHER INFORMATION: In the order of preference, with Val the most preferred
222 <400> SEQUENCE: 9
W--> 223 Xaa Xaa Xaa Leu
224 1
227 <210> SEQ ID NO: 10
228 <211> LENGTH: 10
229 <212> TYPE: PRT
230 <213> ORGANISM: Adeno Virus
232 <400> SEQUENCE: 10
233 Ser Gly Pro Ser Asn Thr Pro Pro Glu Ile
234 1 5 10
237 <210> SEQ ID NO: 11
238 <211> LENGTH: 11
239 <212> TYPE: PRT
240 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
242 <400> SEQUENCE: 11
243 Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu
244 1 5 10
247 <210> SEQ ID NO: 12
248 <211> LENGTH: 10
249 <212> TYPE: PRT
250 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
252 <400> SEQUENCE: 12
253 Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly
254 1 5 10
257 <210> SEQ ID NO: 13
258 <211> LENGTH: 9
259 <212> TYPE: PRT
260 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
262 <400> SEQUENCE: 13
263 Arg Pro Gln Ala Ser Gly Val Tyr Met
264 1 5
267 <210> SEQ ID NO: 14
268 <211> LENGTH: 9
269 <212> TYPE: PRT

RAW SEQUENCE LISTING

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Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

270 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
272 <400> SEQUENCE: 14
273 Phe Gln Pro Gln Asn Gly Gln Phe Ile
274 1 5
277 <210> SEQ ID NO: 15
278 <211> LENGTH: 9
279 <212> TYPE: PRT
280 <213> ORGANISM: Influenza Virus
282 <400> SEQUENCE: 15
283 Ile Glu Gly Gly Trp Thr Gly Met Ile
284 1 5
287 <210> SEQ ID NO: 16
288 <211> LENGTH: 10
289 <212> TYPE: PRT
290 <213> ORGANISM: Influenza Virus
292 <400> SEQUENCE: 16
293 Thr Tyr Val Ser Val Ser Thr Ser Thr Leu
294 1 5 10
297 <210> SEQ ID NO: 17
298 <211> LENGTH: 8
299 <212> TYPE: PRT
300 <213> ORGANISM: Influenza Virus
302 <400> SEQUENCE: 17
303 Phe Glu Ala Asn Gly Asn Leu Ile
304 1 5
307 <210> SEQ ID NO: 18
308 <211> LENGTH: 9
309 <212> TYPE: PRT
310 <213> ORGANISM: Influenza Virus
312 <400> SEQUENCE: 18
313 Ile Tyr Ser Thr Val Ala Ser Ser Leu
314 1 5
317 <210> SEQ ID NO: 19
318 <211> LENGTH: 9
319 <212> TYPE: PRT
320 <213> ORGANISM: Influenza Virus
322 <400> SEQUENCE: 19
323 Thr Tyr Gln Arg Thr Arg Ala Leu Val
324 1 5
327 <210> SEQ ID NO: 20
328 <211> LENGTH: 9
329 <212> TYPE: PRT
330 <213> ORGANISM: Influenza Virus
332 <400> SEQUENCE: 20
333 Cys Thr Glu Leu Lys Leu Ser Asp Tyr
334 1 5
337 <210> SEQ ID NO: 21
338 <211> LENGTH: 8
339 <212> TYPE: PRT

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/31/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence, which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1, 2, 3, 4, 5, 6, 7, 8
Seq#:3; Xaa Pos. 1, 2, 3, 4, 5, 6, 7, 8
Seq#:4; Xaa Pos. 1, 2, 3, 4, 5, 6, 7
Seq#:7; Xaa Pos. 1, 2, 3, 4, 5, 6, 7
Seq#:8; Xaa Pos. 1, 2, 3, 4, 5, 6, 7
Seq#:9; Xaa Pos. 1, 2, 3
Seq#:401; Xaa Pos. 7
Seq#:402; Xaa Pos. 3
Seq#:407; Xaa Pos. 2, 6
Seq#:454; Xaa Pos. 5
Seq#:564; Xaa Pos. 7
Seq#:565; Xaa Pos. 3
Seq#:570; Xaa Pos. 2, 6
Seq#:617; Xaa Pos. 5
Seq#:805; Xaa Pos. 7
Seq#:806; Xaa Pos. 3
Seq#:811; Xaa Pos. 2, 6
Seq#:858; Xaa Pos. 5

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Input Set : D:\SEQLIST 8449-406 (as filed).TXT
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L:51 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:67 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:80 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:84 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:88 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:101 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:105 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:149 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:161 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:179 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:501 M:283 W: Missing Blank Line separator, <400> field identifier
L:4951 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4955 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:401
L:4956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:401 after pos.:0
L:4968 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4972 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:402
L:4973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:402 after pos.:0
L:5037 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:407
L:5042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:407 after pos.:0
L:5652 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5656 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:454
L:5657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:454 after pos.:0
L:7086 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7090 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:564
L:7091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:564 after pos.:0
L:7103 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:565
L:7108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:565 after pos.:0
L:7172 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:570
L:7177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:570 after pos.:0
L:7787 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

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L:7791 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:617
L:7792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:617 after pos.:0
L:10404 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10408 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:805
L:10409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:805 after pos.:0
L:10422 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10426 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:806
L:10427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:806 after pos.:0
L:10496 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10500 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:811
L:10501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:811 after pos.:0
L:11158 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:11162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:858
L:11163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:858 after pos.:0